

SEQUENCE LISTING

SEQUENCE ID NO: 1

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SEQUENCE ID NO: 5, PCR primer

5'-TGGAAGCCAGAGACAAGCAG-3'

SEQUENCE ID NO: 6, PCR primer

5'-AGAAATGGAAGCCAGAGACAA-3'

SEQUENCE ID NO: 7, PCR primer

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SEQUENCE ID NO: 8, PCR primer

5'-CTCAAACACAGGCCTCCGGA-3'

SEQUENCE ID NO: 9, murine Socs2 locus

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DEFINITION Mus musculus Cish2 gene, complete sequence.
ACCESSION AF292933
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE 1 (bases 1 to 13908)
AUTHORS Horvat,S. and Medrano,J.F.
TITLE A 500-kb YAC and BAC contig encompassing the high-growth
deletion
in mouse chromosome 10 and identification of the murine
Raidd/Cradd
gene in the candidate region
JOURNAL Genomics 54 (1), 159-164 (1998)
MEDLINE 99026139
PUBMED 9806843
REFERENCE 2 (bases 1 to 13908)
AUTHORS Horvat,S. and Medrano,J.F.
TITLE Lack of expression of Socs2 causes the high growth phenotype in
mice
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 13908)
AUTHORS Wong,M.L. and Medrano,J.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2000) Department of Animal Science,
University of California, Davis, One Shields Avenue, Davis, CA 95616, USA
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SEQUENCE ID NO: 10, exon 2 probe

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6929	CTCGCCATTA	ACAAATGTAC	CGGTACGATC	TGGGGACTGC	CTTTACCAAC	AAGACTAAAA
6989	GATTACTTGG	AAGAATATAA	ATTCCAGGTA	TAAGTATTTC	TCTCTCTTT	TCGTTTTTTT
7049	TTAAAAAAAAA	AAAAAACACA	TGCCTCATAT	AGACTATCTC	CGAATGCAGC	TAT

SEQUENCE ID NO: 12, 3' Socs2 probe

11185	GGAATTCAAG	TCTACTTGAA	TTAGGTAAAC	TGACAGATTT	AGGGTCCTTA	GGATTAAGTC
11245	TGTGTCTGTT	TCTCTTCTAGT	TCTCTTCAGG	ATTTAAAAAC	CAAAGCCAGT	TCCTAACACC
11305	ACATTTCAAC	ACTTAAAAAA	AAAAAAAAAA	AAAAAAACTT	GTTTATTAA	ACAACCGTAG
11365	GCTCCTTACT	TGCTAGTTA	TGCTCTATTG	GGAAGGAAGA	AAGACAGCCC	TTCTTTAGCT
11425	TGTTTGTGTC	TGAGGGCAAT	CCTTGCACCT	TCGGTTGGT	CTTCTCATTC	TCTCTGCTG
11485	CCCTGGAAGA	TTTCTCCAG	TTTCCCTCT	ATGTGGTTTC	AGAGTAAGTC	ACCTTACCTC
11545	GCACTCAGCT	TAAGGGACAG	CTGTTGTTGG	AGTCAGCCTC	AAAAGCCCC	GTTGTCTCCA
11605	AATGCTGAC	TAGGGGTCA	GCTGAAGCAG	TCATTGTGGT	CTTCCTACCC	ACCTGTCTCT
11665	CAGCTCTGTC	CACAAAGGGAG	GTCTGAGCTG	CCAAGTCTGA	CGGGGGACTC	ACTTCCATAAA
11725	ACATTACTG	AGCCATAAAA	ATAAAACCTGC	TTTTATAGAC	AACTCTCACT	TTGAACCTCCA
11785	TTCTTCACCT	GGAGAAGAAG	GCGCTGCC			

SEQUENCE ID NO: 13, HG deletion breakpoint 5' primer

5' -CTGGGCTCATTGGAAATG-3'

SEQUENCE ID NO: 14, HG deletion breakpoint 3' primer (I)

5' -TATTTCTCCCAATAGCTCG-3'

SEQUENCE ID NO: 15, HG deletion breakpoint 3' primer (II)

5' -CTGGCTTCTGAAAACCTTACC-3'

SEQUENCE ID NO: 16, HG deletion breakpoint 3' primer (III)

5' -GTAGATCTTGGGAGAGGGAGA-3'

SEQUENCE ID NO: 17, HG deletion breakpoint 3' primer (IV)

5' -TGGGCTTCCTTGGGAAAGTT-3'

SEQUENCE ID NO: 18, HG deletion breakpoint 3' primer (V)

5' -AGCTGTCGGCTGAAACGGAG-3'

SEQUENCE ID NO: 19, HG deletion breakpoint 3' primer (VI)

5' -AACGAAGTATCTTGAGTTAC-3'

SEQUENCE ID NO: 20, Merged Consensus genomic sequences of the high growth deletion in mouse chromosome 10.

The sequence covers a region of approximately 659,000 nucleotide bases of genomic DNA. Six BAC clones from the CITB mouse-BAC library corresponding to the minimal path of the physical map of the HG region (Horvat and Medrano, Genomics 54:159-164, 1998) were sequenced. The 6 BACs are: B520, B308, B546, B11I10, B9L14 and B405 and are assembled consecutively in 13 contigs. The contigs have been ordered and separated by sets of 20 Xs that identify gaps in the sequence.

The approximate location of the hg deletion is from nucleotide position 63,724 to 533,100. The breakpoint of the deletion is in position 63,724 occurred in intron-2 of the mouse *Socs2/Cish2* gene (Accession # AF292933). The deletion of exon 3 of this gene eliminates the expression of this gene in hg mice and appears to be the causative reason of the high growth phenotype.

The deletion breakpoint at position 533,100 was determined because after this position is the sequence of the *Vespr* (viral encoded semaphorin receptor) gene (mRNA seq. Accession # AF190578), which is fully expressed in hg.

The deletion encompasses the full-length sequence of the RAIDD/CRADD gene (Accession # AJ224738) (from nt 146,837 to 298,188).

DEFINITION test, 659158 bases

ORIGIN

1	CTTGATGGAG	TCGGTTGGGG	TTTTTTGTTT	GTTTGTGTTG	TTGTTTTCTG
51	GAAAGTTGAT	AAACTTAATG	AGGACATGGC	TTGCAGCGTG	GCAGGCACAA
101	CACCTGATGC	TAAGGTCCTG	ACTAATTCA	TGCTCAGAGG	TATTATTCC
151	AGTAACAGGA	GCCAATTCCA	CGTGCAGT	TGTTTACAGC	ACTGTGCTAT
201	CACAGAGGCG	CATGCGCAGT	TTGGAGGGAA	GTGTCCGGTT	GCTGTTCC
251	TGCTGTGTAT	TGGCTGGGGT	AAGCACCATG	GCTTCAGGT	CTGTTAAGAG
301	TGACCCAAGC	GCATGAGCAT	TGGAGACAGC	AGTGCCCGAG	CTGTTGTCAGT
351	GTTGAAACCA	GACTACAAACG	CAGGAGAAAG	GACTCTGAAG	TCGACATTG
401	CTCTAGCTGT	CAAGATGATA	AAAAAATAAG	ACAATAGATG	TTGGTAAACT
451	GTCAGCTGAA	GAAGTAGAAA	TGGCCACCC	AAGGAGAGAA	TGGAATGCC
501	GTGAGCATGG	TCCTCAGGCA	AAGGAAGTGG	AACAGTTGAC	CAAAACCAA
551	GAAGAGGTAG	AAGGGAAATC	TCAGCAGGAG	AAGGAGAGGG	AATGGAAAGG
601	AGAAAATAGAC	AAAATCGTGG	ATTTTATAAC	TCCCGAGAGG	CACCAATTCT
651	GTTAGAAGCC	GTCCTGGCCT	TTCACTCCGG	AAAGGTTTC	TTGTTTTTC
701	TTTTTTAAGT	TGCCCATCAG	GGAATTAGGC	CATTAATACT	GAATCGGATC
751	CTTGTCTGTC	CAGTTGGGTG	CTTTATTGTA	ATGATGGACA	TCTTTATAAA
801	CATCTTAATC	TTAATACATA	ACTTTTGGA	ATAAAACCTA	GACTGACAAA
851	AACAGAATAG	TGAACAAAAG	AGAAGAAGGT	TAGCAATAAT	TGACAGTAAT
901	GTGAACCTCT	TGCCCAATGG	GAGCACCTAG	GTTCTCTCTC	TTTTTTTTAT
951	TGCATCAAAG	AAAGTAAGTC	TGATACAAGC	TTGTCAGATA	TACCAACTTT
1001	GCTCCTAACT	TTAAAAACACT	ATTAGTCTTT	TTCAAATTAA	TACCGAACAA
1051	AGCTATTAT	TTGACGGACA	AGTTGTATAT	TGACTTATCT	GAACAAGCTA
1101	TTTCTATTGA	AAAAAATTAT	ATTGACTTAT	AATAAAAGTT	TTACAAGATC
1151	AAGATAAGTT	ATGAGCATGA	AAGAACAAAGG	CTTGTAAAGTA	AAATTAAATA
1201	ATTAAAAAGT	GTTCCTGTGA	GTCCAGAGTT	GACCAATGTG	GAACCTCTAGA

1251 AGGCCAAACG CAGTCCTGTG TGAGTACTTT AGCAAATTAG ACTTTAATGT
 1301 ATTGAAAATA TAGATTAAATG TAGTCCTGA ATTATGTCTT TTTTTGTTTG
 1351 TTTGTTTGT TTTGTTTTT TTTTCGAGA CAGGGTTTCT CTGTGTAGCC
 1401 CTGGCTATCC TGGAACTCAC TCTGTAGACC AGGTGGCCT TGAACTCAGA
 1451 AATCCGTCTG CCTCTGTCTC CTGTGTGCTG GGATTAAGG CGTGCAC
 1501 CACGCCCGGC TCCGAATTAT GTCTTCATG TGTTGCTGAT TTTGAGTTT
 1551 CTAACAAAT AGTAACCCAT CACAGCTTA CTTCTCTGT ATCTTCCTAT
 1601 CTCTCCATG GCTGAGACAA AACTATTAC TTCCTCACTA CCCTCTATG
 1651 AAAAACACT TACAGGTTT AGTGGCCATT TACAATTACA TGTGAGGGAT
 1701 GCTACTTTAA AAGCAGCCT AGGAAGAGCC GGAGAGGCTG TGTTGCCTA
 1751 ACCTGCGGAA CACATTCTCG ACAGAACCGC CAGAGGGCAC TGTGACACAG
 1801 CATTCAAGCCT GAACCGCTTA CCCTGTGGT GTGACTTGA AATGCCAGAA
 1851 TGGCAGAGAA TTTGAACATT GCTACTTGAG AAAGGGTGGT TTGATAATGT
 1901 CATTGCCGGA AGTCGTTCTA CTCGTCTATC ATTAAGTATT TATACAACAG
 1951 CTGGTTGTGA GAAGATCTG TTTCTAGCTG GCCAACTCAA ACATCCTAA
 2001 GATCAGTGCT ACTTGCTAAA TATCGGCCGT GCTACTTATA TTTTCTAAT
 2051 GACATTCCC ACTGTGGATG TTTTCACTA TCATTTTTT TAATTAAGTT
 2101 TAGGTAGAAA ACCTTGACTT ACTCAAAGAT AACATTGTTA ACTGTTTTG
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 2201 TTTCTTTTG TTAGAAAATA TGTTTTTT TAAAGATTT TCTTTAATG
 2251 TGTATGGATG CTTTCGTTGC AGGTGTGTCT TAGTAACATG TGGGTGTCTG
 2301 GTGCCCTTGT ATCTCTGGG ACTGTAGTTA CAGACAGCTG GGAACGTACT
 2351 GACATGTGGT GCTGGGAATT GAACTCAGGT CCCCTGGGAG AGCAGCCAGT
 2401 GCTCTTGACT ACTGAGCCAT CTCTCCAGCC CTTGTACTTT CTTTTGTTT
 2451 TTAATTTAA ATGGTGTGTG TTGTTTGTCT CTCGTCTCTC CACATGTGTC
 2501 TGTCGTGTG TATGTTGTCT GTCTGTCTGT CTCTCCGTGT GTGTGTGTG
 2551 GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT TCTGTTGGGG ACTGATCTCA
 2601 GGGCTTTCTT TATACATGTC AGGCAAGCAC TGTGCCTCTG AATTGCCTCC
 2651 TCACAAGGGC TAAGGGTTT GTGACTCCTT CTTTGGTCC CACAAACTCC
 2701 TGCCCTCCTA AGAAGCTAAC AACTCTAGTC CCAGTCAGCA GAGGTAAGAG
 2751 AACCCATTAG TTAAGACTCT TGATTTCCAG GCCAAGAAAG CCCATCCATC
 2801 CACAGTAGAG TCCAGCAATG GGAGTCTGTT GGAGGAGGAT CACAGGACTG
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 3151 GGGAGTTAAG TTTCAAGGCC TGAACTCAGG TCATCAGGCT TATACAGCAA
 3201 GCACCTTTAC CCATCAACCA GTTGACGTGC CCATTGTTAA GCTGCTTGCC
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 3301 GTCATCGTC TCGTTGTTT TGAGATGAGG TCTCATAGCT CTAGCAGGCC
 3351 TAGAACTTAC TGTGTAGGCC AGGCTGGCCT CTGTTTCCCAGTGTGAGT
 3401 TTGAAGGCAT GTGCCACCAT GCAGGGCGGT TAGGCATCTT CTAGTGTGGT
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 3751 TATTTTATAT CTCTCCTCAA CTTTACCTGC CTGCACTAA TCACTTAGTA
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 3851 AGGAGACATC TTTATCTTA ATTCCAACCA TATTTTTATT TGTGTGTGTG
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4351 TGAGACAGGA TCTCTCATAG TGTCTGTCGG TCTCCACCCC CAAGTGCCTGG
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 11401 CTTAATTTCG GTAAGTGTCC CCAACATCTC ATTCAAAATG GCATAGAACAA
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 11501 AAAATGACTC GTGCTTATA TGTAACTTG GGCTACATCT ATCCAAGGCA
 11551 GGCCCCAAGC ATCCTTATT TTTTATTAT TTACTTATT TTATATAGAC
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